APPLICATION OF MARKER ASSISTED SELECTION TO IMPROVING A QUANTITATIVE TRAIT IN COMMON BEAN

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Since marker assisted selection (MAS) has proven successful for improving qualitative traits (Haley et al, 1994; Miklas et al. 1993; and Young et al., 1996), we proposed to further apply this to the improvement of a quantitative trait. To improve a quantitative trait such as yield performance under moisture stress in common bean, phenotypic selection cannot begin until the F_6 generation where sufficient homozygosity and seed is available for replicated trials. If RAPD markers could be identified that explained a significant amount of the variation for this trait, selection could begin in early generations such as the F_3 or F_4 or, alternatively, selection could be performed in locations where drought is not present.

Two recombinant inbred populations were developed from crosses between Sierra, a Michigan adapted pinto variety, and two drought tolerant Mexican breeding lines (AC1028 and Lef-2RB). Individual F_2 plants were advanced to the F_5 generation by single seed descent where seed from individual F_5 plants was bulked to create 78 recombinant inbred lines (RILs) in the Sierra/AC1028 population (S/A) and 95 RILs in the Sierra/Lef-2RB (S/L) population. The two populations were grown in seven locations in Michigan and Mexico (1990-1994) under two moisture regimes (stress and non stress). Yield data from the first four years and five locations were used to identify RAPD markers associated with drought resistance and the data from two 1994 Mexican locations was used to test the effectiveness of MAS vs. conventional phenotypic selection.

For the marker analysis, the three parents were screened with 600 random decamer primers, 50% of which were polymorphic Of these polymorphic markers, 70 were chosen to run against each population. One way analyses of variance were performed between marker data and yield data [yield under stress (Yd), yield under non-stress (Yp) and the geometric mean between the two treatments (GM)]. These analyses were performed on yield data from each location, separately, and on data from a combined analysis over all locations (1990-1993). No single RAPD marker was observed to be consistently significant over locations. In fact, only 3% of the RAPD markers were significantly associated with Yd, Yp, or GM in three environments and none in four. We felt that because of the strong environmental influence on yield performance under stress, a RAPD marker may be significantly associated in one environment while an adjacent marker would be associated in another environment. Thus it would take a region of the genome to absorb the environmental error. Mapmaker was used to determine if any of the RAPD markers were associated in linkage groups.

In S/A, 42 of the RAPD markers were associated in nine linkage groups and in S/L, 34 of the markers were associated in 10 linkage groups. None of the RAPD markers was more than 10 cM from its neighbor at a LOD score of 4.0. Multiple regression analysis was performed between all markers from each linkage group and yield data to determine if a region of the genome could better explain the variation for yield performance under stress. Linkage group one, consisting of five RAPD markers ($OA08_{780}$, $OA04_{560}$, $OX11_{680}$, $OZ08_{750}$ and $OX18_{980}$) was determined to be consistently associated with Yd, Yp, and GM across locations and explained as much as 62% of

the variation for yield performance. Using these markers 34 RILs and Sierra were identified as a potentially above average genotypic group (PAA) and 27 RILs and Lef-2RB were identified as a potentially below average genotypic group (PBA). Using the same selection intensity, 35 RILs were identified as an above average genotypic group (AA) based on yield performance combined over four years and five locations (1990-1993) and 28 RILs were selected as a below average genotypic group (BA). Conventional phenotypic selection was performed in this manner based on Yd, Yp, and GM

Using yield data combined over the two 1994 Mexican locations (Madero, Dgo. and Calera, Zac.) orthogonal contrasts were performed on the contrasting genotypic groups from each selection criterion (MAS, Yd, Yp, and GM) Marker assisted selection in S/L demonstrated significant differences between genotypic groups where PAA out-yielded PBA by 15 g m^{-2} under stress and 17 g m^{-2} under non stress. Conventional, phenotypic selection, however, based on Yd, Yp, or GM was not effective in improving AA over BA in S/L. Selection based on marker genotype improved PAA by 13 g m^{-2} above the experimental mean whereas the mean of PBA was only 2 g m^{-2} below the experimental mean. Selection based on Yd, Yp and GM, however, did not improve AA above the experimental whereas selection based on Yd or GM resulted in mean values of BA that were 9 and 7 g m^{-2}, respectively, below the experimental mean. These results suggest that MAS may be a better indicator of improved performance while phenotypic selection is a better indicator of below average performance which could be used to rogue individuals from a population.

Since MAS proved effective in S/L, these markers were used to select RILs in S/A. Twenty-six RILs and Sierra were identified from S/A as a PAA group whereas 22 RILs and AC1028 were selected as a PBA group. Marker assisted selection was compared to conventional, phenotypic selection in the same manner as was performed in S/L. Selection based on markers in S/A was not effective in improving PAA over PBA. In fact, PBA out-yielded PAA by 4 g m^{-2} under stress and 7 g m^{-2} under non stress. Phenotypic selection, however, demonstrated a significant difference between AA and BA with a gain in performance of up to 8 g m^{-2} above the experimental mean for stress conditions and 19 g m^{-2} above the experimental mean for non stress. Clearly, MAS was not effective in improving yield performance under moisture stress in S/A. Since heritability estimates for yield in S/A were three times greater than S/L (Schneider, 1995), these results support the conclusion that the effectiveness of MAS on a particular trait is inversely proportional to the heritability of that trait (Lander and Botstein, 1989).

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